

OVERCOMPLETE BASIS TRANSFORM-BASED MOTION RESIDUAL FRAME CODING METHOD AND APPARATUS FOR VIDEO COMPRESSION

FIELD OF THE INVENTION

- 5 The present invention pertains to the field of compression and in particular to video compression methods and apparatuses.

BACKGROUND

10 A sequence of pictures can occupy a vast amount of storage space and require very high transmission bandwidth when represented in an uncompressed digital form. Point to point digital video communication became practicable several years ago following advances in computer networks and signal compression technology.

The standardization effort for digital video compression was initiated in approximately 1988. Currently, the Moving Picture Experts Group (MPEG) committee under ISO/IEC
15 has completed both the MPEG-1 and the MPEG-2 standards; the MPEG-4 standard has also been completed, but new proposals are still being accepted. In addition, CCITT developed a series of recommendations – H.261, H.263 and H.263+ – that focus on low bit rate applications. All of these attempts at standardization utilize a two-step procedure to compress a video sequence. The first step uses a motion estimation and
20 compensation algorithm to create a predicted video frame for the current video frame using the previous video frame, wherein the difference between the current video frame and the predicted video frame is computed and is called the motion residual picture (MRP). The second step in the standard procedure is to code the MRP using the Discrete Cosine Transform (DCT). Such DCT-based systems do not perform well in all
25 circumstances. At the low bit rates needed for personal video communication, DCT-based systems cause noticeable distortion and visible block artifacts. For high visual quality applications, such as DVD, the compression ratio achieved can be quite low.

Motion residual pictures can be coded using other transform-based techniques. For
30 example, discrete wavelet transforms (DWT) and overcomplete basis transforms can

also be used. Zakhor and Neff presented a motion residual coding system in U.S. Patent No. 5,699,121 based on an overcomplete basis transform algorithm called matching pursuit. This was first proposed by Mallat and Zhang in *IEEE Transaction in Signal Processing*, vol. 41, No. 12, Dec. 1993. Zakhor and Neff's video coder improves both
5 the visual quality and the PNSR over standard DCT-based video coders. However, their system is very slow and the compression performance is not optimized due to an ad-hoc design for matched basis position coding and quantization of the transform coefficients. Therefore there is a need for a new overcomplete transform based video coding technique that can provide both speed and efficiency.

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This background information is provided for the purpose of making known information believed by the applicant to be of possible relevance to the present invention. No admission is necessarily intended, nor should be construed, that any of the preceding information constitutes prior art against the present invention.

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SUMMARY OF THE INVENTION

An object of the present invention is to provide a overcomplete basis transform-based motion residual frame coding method and apparatus for video compression. In accordance with an aspect of the present invention, there is provided a method for encoding a residual image using basis functions from an overcomplete library, said
20 method comprising the steps of: obtaining the residual image, said residual image having a size and an energy; and decomposing said residual image into a list of one or more atoms, each atom representing a basis function from the overcomplete library, said step of decomposing said residual image including the steps of: (i) identifying a replacement region in the residual image for representation by an atom using a residual
25 energy segmentation algorithm; (ii) creating a subset of basis functions from the overcomplete library, each basis function in the subset matching with the replacement region within a predetermined threshold; (iii) identifying an atom within the subset of basis functions, said atom for representing the replacement region and said atom having parameters; (iv) quantizing said atom and modifying the parameters of the atom into a form suited for encoding; (v) encoding said quantized atom, subtracting said atom from
30 the replacement region in the residual image thereby reducing the energy of the residual image and using a quadtree-based atom coder to reduce the size of the residual image; and (vi) comparing the reduced size of the residual image or the reduced energy of the

residual image with a predetermined criteria and repeating steps (i) to (vi) until the predetermined criteria is achieved; thereby encoding said residual image and reducing the size thereof to a predetermined level.

- 5 In accordance with another aspect of the present invention there is provided an apparatus for encoding a residual image using basis functions from an overcomplete library, said apparatus comprising: means for obtaining the residual image, said residual image having a size and an energy; and means for decomposing said residual image into a list of one or more atoms, each atom representing a basis function from the overcomplete library, said means for decomposing said residual image including: (i) means for
10 identifying a replacement region in the residual image for representation by an atom using a residual energy segmentation algorithm; (ii) means for creating a subset of basis functions from the overcomplete library, each basis function in the subset matching with the replacement region within a predetermined threshold; (iii) means for identifying an
15 atom within the subset of basis functions, said atom for representing the replacement region and said atom having parameters; (iv) means for quantizing said atom and modifying the parameters of the atom into a form suited for encoding; (v) means for encoding said quantized atom, subtracting said atom from the replacement region in the residual image thereby reducing the energy of the residual image and using a quadtree-
20 based atom coder to reduce the size of the residual image; and (vi) means for comparing the reduced size of the residual image or the reduced energy of the residual image with a predetermined criteria; thereby encoding said residual image and reducing the size thereof to a predetermined level.
- 25 In accordance with another aspect of the present invention there is provided a computer program product comprising a computer readable medium having a computer program recorded thereon for performing a method for encoding a residual image using basis functions from an overcomplete library comprising the steps of: obtaining the residual image, said residual image having a size and an energy; and decomposing said residual
30 image into a list of one or more atoms, each atom representing a basis function from the overcomplete library, said step of decomposing said residual image including the steps of: (i) identifying a replacement region in the residual image for representation by an atom using a residual energy segmentation algorithm; (ii) creating a subset of basis functions from the overcomplete library, each basis function in the subset matching with

the replacement region within a predetermined threshold; (iii) identifying an atom within the subset of basis functions, said atom for representing the replacement region and said atom having parameters; (iv) quantizing said atom and modifying the parameters of the atom into a form suited for encoding; (v) encoding said quantized atom, subtracting said atom from the replacement region in the residual image thereby reducing the energy of the residual image and using a quadtree-based atom coder to reduce the size of the residual image; and (vi) comparing the reduced size of the residual image or the reduced energy of the residual image with a predetermined criteria and repeating steps (i) to (vi) until the predetermined criteria is achieved; thereby encoding said residual image and reducing the size thereof to a predetermined level.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 illustrates the overall diagram of video compression systems that use the over-complete basis transform and associated coding methods according to one embodiment of the present invention.

Figure 2 is an example of a motion residual image processed by one embodiment of the present invention.

Figure 3 illustrates a simple dictionary with 16 bases for use with one embodiment of the present invention.

Figure 4 describes the whole atom decomposition process based on over-complete basis according to one embodiment of the present invention.

Figure 5 describes the basic steps executed by the residual energy segmentation algorithm (RESA) according to one embodiment of the present invention.

Figure 6 illustrates the first step of RESA according to one embodiment of the present invention.

Figure 7 illustrates the second step of RESA: the horizontal growing scheme, according to one embodiment of the present invention.

Figure 8 illustrates the third step of RESA: the vertical growing scheme, according to one embodiment of the present invention.

Figure 9 describes the matching pursuit atom search using the progressive elimination
5 algorithm (PEA) according to one embodiment of the present invention.

Figure 10 illustrates how to form the sub dictionary of matching basis and searching position candidates according to one embodiment of the present invention.

10 Figure 11 illustrates the fast calculation of region energy according to one embodiment of the present invention.

Figure 12 illustrates the parameters for one atom according to one embodiment of the present invention.

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Figure 13 is an example of an atom position map according to one embodiment of the present invention.

Figure 14 is a flowchart illustrating the atom encoding process according to one
20 embodiment of the present invention.

Figure 15 is a flowchart illustrating the decoding of a compressed residual signal according to one embodiment of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

25 The current invention is an new coder for overcomplete-transform based residual picture coding, used for motion compensated video compression systems. This invention is analogous to previous matching pursuit video coders in that they decompose the residual image into a list of atoms, which represent basis functions from an overcomplete dictionary. The atom finding process, however, is performed using a Residual Energy
30 Segmentation Algorithm (RESA) and a Progressive Elimination Algorithm (PEA). The basis dictionary can be very large in order to characterize the features appearing frequently in motion residual images. To find an atom, RESA identifies the approximate shape and position of regions with high energy in the motion residual

images such that a good match can be found by comparison with a smaller subset of bases within the dictionary. Furthermore, PEA progressively removes pattern candidates from consideration by pre-computing the energy of search windows, thereby reducing the computation time needed to find the best match. Whenever a matched
5 atom is found, the residual image is updated by removing the part characterized by the atom. The foregoing steps of finding atoms and updating residual images are repeated until the desired compression bit rate or quality has been achieved.

The invention introduces a new modulus quantization scheme for matching pursuit with
10 an overcomplete basis, that changes the atom finding procedure. The coefficients produced directly from the transform are continuous floating-point values, which require quantization for optimal digital coding under a bit budget. In the matching pursuit algorithm, it is necessary to use an in-loop quantizer – where each found atom is first quantized, and then used to update the residual image. As such each atom affects the
15 selection of subsequent atoms. If the quantizer is specified before coding begins, as in previous matching pursuit methods, it is difficult to optimize the quantization scheme as the optimal quantizer design depends on statistics of the list of chosen atom moduli. The quantization scheme according to the present invention chooses the quantizer adaptively during the atom searching process.

20 In addition to the atom modulus, the index of the chosen basis and the position of the atoms need to be transmitted in an overcomplete-transform based coder. The invention includes a method to code the atom position information efficiently. The atom position distribution forms a 2D map, where pixel values of one and zero represent the presence
25 of atoms or lack thereof in each position respectively. A quadtree like technique enables coding of the position map. The modulus and basis index information are embedded in the position coding. The atoms for different channels of color video (Y, U, V) are coded independently.

30 All atom parameters are transmitted after they have been encoded into a compressed version of the residual images. For the decoding process, the decoder reconstructs the residual image through interpreting the coded bit stream back into atom parameters and combining the atom information to form the reconstructed stream of residual images that

are then combined with the motion compensated image to form the reconstructed video stream.

5 The present invention is a method for encoding motion residual images comprising the steps of: forming the atom decomposition of the residual image in an overcomplete basis space using the modified matching pursuit algorithm; choosing the modulus quantizer; coding the atom position map, modulus as well as the index for the selected basis. The present invention further provides a method for decoding residual signals that have been encoded using the above encoding method.

10 Figure 1 illustrates the associated processing executed by a video compression apparatus 10 that employs the residual image coder 20 according to one embodiment of the present invention. The video frame is initially processed by a motion estimator 30, which compares the current frame with one or two reference frames. In most cases, 15 objects in the video change their position in successive frames while the background remains the same. Since the reference frames have been transmitted to the video decoder 12, some regions in the reference frame can be used to construct the current frame. The motion estimator 30 identifies those regions within the reference frames that are similar to regions within the current frame. The motion compensator 32 produces 20 the difference between those similar regions and combines them as a motion residual image. The position relationships between similar regions are represented as motion vectors, which are processed by the motion vector encoder 34. The atom decomposer 40 processes the residual image first, and then the atom encoder 42 compresses the resulted atoms. The coded motion vectors and atoms are combined into one bit stream by the 25 multiplexer 22. The compressed video is transmitted or stored by apparatus 24, which can deliver the video in compressed format to the video decoder 12.

The lower part of Figure 1 illustrates the decoder 12, in which the demultiplexer 26 30 separates the compressed video signal, sending corresponding bits to the motion vector decoder 36 and the residual image decoder 28, respectively. The motion reconstructor 38 forms the prediction frame from the reference frame and the motion vector. The residual image decoder 28 reconstructs the residual image. These two signals, namely the prediction frame and the residual frame are added together to generate the final reconstructed video frame.

Figure 2 is an example motion residual image for the Y colour channel. The original residual image has both negative and positive values. For proper displaying of the residual image as a 256 level gray image, the pixel values in the residual image are shifted and scaled so that pure gray means zero, while black and white represent negative and positive values, respectively. For example, the residual image comprises several high-energy regions, which correspond to the motion of objects in the video.

Most signal compression techniques transform the original data into some more compact format through different kinds mathematical transformations. Some mathematical transforms, such as DCT and DWT, use a complete basis, which forms an invertible transformation matrix. Recently, overcomplete basis and associated transformation algorithms have received considerable attention. The number of bases in an overcomplete basis dictionary is much larger than the dimension of the original data. The benefit of an overcomplete basis is that the transformed coefficients are more effective in representing the true features in the original signal. There exist many mathematical methods to build a basis dictionary for different signals. Several dictionaries for video motion residual pictures have been designed and have been proven to cover the features in residual pictures well. For example, a basis dictionary based on separable Gabor functions has been described by Neff and Zakhor in "Very Low Bit Rate Video Coding Based on Matching Pursuits", IEEE Transactions on Circuits and Systems for Video Technology, Feb. 1997, 158-171, and a basis dictionary based on Haar functions has been described by Vleeschouwer and Macq in "New dictionaries for matching pursuit video coding", Proc. of the 1998 International Conference on Image Processing, vol. 1, 764-768. Figure 3 is a simple example dictionary containing 16 bases. Any of the above dictionaries can be used with the present invention. Having particular regard to the above-mentioned Gabor dictionary, there are 400 2D functions explicitly mentioned. However, it actually includes many more basis structures implicitly since each of those 400 2D functions can be placed at every possible position within the image. Using a frame size of 176X144 pixels implies that the dictionary actually contains $400 \times 176 \times 144 = 5.7$ million bases structures – which makes it highly overcomplete. The transformation directly using the "matching pursuit algorithm" described by S. Mallat and Z. Zhang in "Matching Pursuits With Time-Frequency Dictionaries", IEEE Transaction in Signal Processing, vol. 41, No. 12, Dec. 1993, will

take an extremely large number of computations to determine the transform coefficients. The matching pursuit for video compression, invented by Zakhor and Neff in US Patent No. 5,699,121, reduces the calculation burden, however it remains computationally expensive. The present invention provides a way to transform residual images based on
5 general dictionaries, which is performed by the atom decomposer 40, and a way to code the transformed coefficients, which is the task of the atom encoder 42.

The operation of the atom decomposer 40 is fully described in Figure 4, according to one embodiment. The first step (block 61) executed by the atom decomposer 40 is to
10 find the initial search region. This step is realized by the residual energy segmentation algorithm (RESA), wherein one embodiment thereof is shown in Figure 5. RESA is based on a general region growing idea. It initially selects a 2x2 block as a starting point for region growing (block 70). This step requires the division of the residual image into 16x16 blocks, as shown in Figure 6. The energy, which is the sum of the square of all
15 pixel intensities, is computed for each block, and the block with the highest energy is identified as block 71 shown in Figure. 6, for example. Block 71 is further divided into four 8x8 sub-blocks, and the sub-block 72 with the highest energy is identified. Within that 8x8 sub-block 72, the highest energy 2x2 block 73 is also identified, wherein this block will be used as the starting point for region growing.

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The next step of RESA (block 74 illustrated in Figure 5) is to check the 2x2 block in the left side of the current region. Figure 7 illustrates this step of RESA. A threshold is calculated dynamically as:

$$T = AE * \max(7 - AU, 5) / 10$$

25 where AU is the number of blocks that have been added on the left side of the start block, and AE is the average energy per 2x2 block of the current region. If the energy of the checked 2x2 block is larger than the current threshold, the tested 2x2 block is grouped with the current region, together forming a new larger current region. Otherwise, a stop point has been found on this side, and we do not group the blocks
30 together. In a similar, symmetric fashion, check the 2x2 block on the right side of the current region. Continue growing first the left side and then the right side, until stop points are found on both sides or the width of the rectangle has reached 32, (whichever

comes first). A horizontal strip rectangle 75 is formed after this step, wherein the dimension of the strip is $2*2m$, $1 \leq m \leq 16$.

The final step of RESA (block 76 in Figure 5) is to grow the region vertically based on strip 75, as shown in Figure. 8. Assume the width of the strip 75 is W . Consider the $2*W$ strip rectangle above the current region, together with a threshold:

$$Ts = AEs * \max(7 - AUs, 5) / 10$$

where AUs is the number of $2*W$ rectangles that have been added above the initial strip and AEs is the average energy per $2*W$ rectangle included in the current region. If the tested $2*W$ rectangle has an energy that is larger than a threshold, merge it into the current region. Otherwise, a stop point has been found on this side. In a similar, symmetric fashion, check the $2*W$ rectangle below the current region. Continue growing first above and then below, until stop points are found on both sides or the height or the current region has reached 32, (whichever comes first). In the end we obtain a rectangle 77 that has dimension $2n*2m$, $1 \leq n, m \leq 16$.

With further reference to Figure 4, the process for finding the closest matched basis from the given dictionary is illustrated (block 62). The degree of matching between a basis and the residual image is represented by the absolute value (modulus) of their inner product, which is called the atom modulus, wherein a large modulus implies a good match. The process of determining this modulus requires computing a number of inner products, and selecting the one with the largest modulus as the current atom. This process can be the slowest part of the matching pursuit algorithm. In the classical matching pursuit algorithm, the inner product between the residual image and each of the millions of elements in the dictionary would need to be computed to determine the modulus. In the prior art for example, the $16*16$ block with the highest energy in the residual image is simply selected as the initial search region - each basis structure is centered at each location in the chosen block, and the inner product between the basis structure and the corresponding residual region will be computed. For a dictionary with 400 basis, this process requires $256*400=102400$ inner product calculations. Figure 9 illustrates the new matching pursuit process according to the present invention.

The resulting RESA rectangle 77 in Figure 8 provides an initial estimation for the shape of the high-energy feature. It is used to filter out bases in the dictionary that have a shape that is too different from the RESA rectangle. A subset of matching basis candidates (block 80) is then formed. Assume the width and height of rectangle 77 is w and h respectively, a sub-dictionary is formed containing all bases with shapes, specified by *width* and *height* respectively, that satisfies:

$$w-tw1 \leq \text{width} \leq w+tw2 \text{ and } h-th1 \leq \text{height} \leq h+th2$$

where $tw1, tw2, th1$ and $th2$ are values set to confine the basis size. These values may be changed and adjusted according to the dictionary structure. The largest and smallest sizes of tested bases are illustrated as rectangle 90 and 91 illustrated in Figure 10. For example, block B80 is a simple sub-dictionary example containing four bases.

RESA can further estimate the location of high-energy features in the residual image. The position candidates for matching bases are selected around the center of the RESA rectangle 77 (block 81). Figure 10 shows a small rectangle 92 whose center is the same as RESA rectangle 77. It is supposed that all pixels within rectangle 92 will work as a center for the tested residual region. Rectangle 94 in Figure 10 is an example whose center is point 93, or the left-top corner of rectangle 92. The width (ws) and height (hs) of rectangle 92 is supposed to be variable with RESA rectangle 77. The relationship is:

$$ws = 2 * \min(w/2 + 1, 6) \text{ and } hs = 2 * \min(h/2 + 1, 6)$$

The size of rectangle 92 can be decided by other rules or simply be fixed in an implementation. The basic idea is that a good match is located around the center of the RESA rectangle 77. Furthermore, any positions within rectangle 92 that already contain the center of an atom will not be considered for any new atoms. Point 95 in Figure 10 is an example. It should be noted that the prior art does not place such a restriction. The idea for this type of restriction is that if one atom provides a good fit, it should remove the energy around its center without introducing too much extra energy at its boundary. As such it is not desired for the matching pursuit algorithm to return to the same position to produce a second atom. This restriction of forcing no position repetition has almost no effect on coding performance and can make the coding of the atom position information simpler.

The next processing step (block 89 in Figure 9) is called the progressive elimination algorithm (PEA) for the residual matching pursuit. It is independent of the method used to form the testing basis sub-dictionary and set of testing positions. For example, PEA will still operate if the sub-dictionary is the entire dictionary, and the set of position candidates is the set of coordinates comprising the whole residual image. PEA is a method of finding the closest matching basis more efficiently by progressively removing comparison candidates from consideration. This contrasts with classical matching pursuit, which compares all basis candidates at all possible positions. Initially the maximum modulus M_m is set to be zero (block 82). Next a basis $b(k,l)$ is considered (block 83), where k and l represents the width and height of the 2D basis function. A same sized region centered at one position candidate $r(k,l,p)$ in the residual image is formed (block 84). Block 85 compares $\|r(k,l,p)\|$, the energy of $r(k,l,p)$, with the current maximum modulus (M_m) to decide if there is a need to calculate the inner product between $r(k,l,p)$ and $b(k,l)$. In order to explain this operation, recall the mathematical triangle inequality:

$$|\langle r(k,l,p), b(k,l) \rangle| \leq \|r(k,l,p)\| \|b(k,l)\|$$

The objective of matching pursuit is to find the maximum $|\langle r(k,l,p), b(k,l) \rangle|$. Assume the current maximum modulus is M_m . If, for basis $b(k,l)$ at position p , the corresponding residual $r(k,l,p)$ satisfies $\|r(k,l,p)\| \|b(k,l)\| \leq M_m$, then:

$$|\langle r(k,l,p), b(k,l) \rangle| \leq \|r(k,l,p)\| \|b(k,l)\| \leq M_m$$

In this case, it is unnecessary to calculate the inner product $\langle r(k,l,p), b(k,l) \rangle$, and the region $r(k,l,p)$ is moved to the next position. The norm of basis $\|b(k,l)\|$ can be calculated a priori (actually most of the basis are normalized, namely $\|b(k,l)\|=1$), the only overhead for this test then is to calculate the energy of $r(k,l,p)$. An effective algorithm to determine $\|r(k,l,p)\|$, is described below.

Assume there are n different sizes of basis heights $\{v_1, v_2, \dots, v_n\}$, and m different sizes of basis widths $\{h_1, h_2, \dots, h_m\}$, that are increasingly ordered. The search rectangle dimension is $h_s \times w_s$, and the left-top point of the search rectangle is $p(x,y)$. The $h_s \times w_s \times n \times m$ energy values can be calculated through the following four steps:

Step 1: Calculate the energy for the $s=h_m+k$ columns (Figure 11 shows an example of the columns). These columns are centered at $(x-h_m/2+i, y)$, $i=0,1,\dots,s-1$. Their height is v_1 . Their energy is represented as $C_{1,0}(0), C_{1,1}(0), \dots, C_{1,s}(0)$, and calculated as:

$$5 \quad C_{1,i}(0) = e(x-h_m/2+i, y-v_1/2) + \dots + e(x-h_m/2+i, y) + \dots + e(x-h_m/2+i, y+v_1/2)$$

where $e(x, y)$ represents the energy of pixels at position (x, y) .

The energies for the next s columns with same coordinates as above strips and length v_2 can be computed as:

$$10 \quad C_{2,i}(0) = C_{1,i}(0) + \text{Extra } (v_2-v_1) \text{ Pixels Energy, } i=1,2,\dots,s$$

Generally, we have:

$$C_{j,i}(0) = C_{j-1,i}(0) + \text{Extra } (v_j-v_{j-1}) \text{ Pixels Energy, } i=1,2,\dots,s; j=1,2,\dots,n$$

Step 2: Calculate energy of columns that are vertical shift of columns in Step 1, using:

$$C_{j,i}(a) = C_{j,i}(a-1) - e(x-h_m/2+i, y-v_1/2+a-1) + e(x-h_m/2+i, y+v_1/2+a), a=1,\dots,hs$$

15 where a represents the vertical shift number corresponding to y .

Step 3: Calculate the energies of regions with height v_j , ($j=1,\dots,n$) and width h_1, h_2, \dots, h_m and center $(x, y+a)$, ($v=0,1, \dots, hs$) using:

$$20 \quad \begin{aligned} S_{j,1}(0,a) &= C_{j,(h_m-h_1)/2}(a) + \dots + C_{j,h_m/2}(a) + \dots + C_{j,(h_m+h_1)/2}(a) \\ S_{j,2}(0,a) &= S_{j,1}(0,a) + \text{Extra } (h_2 - h_1) \text{ columns' energy} \end{aligned}$$

Generally,

$$S_{j,i}(0,a) = S_{j,i-1}(0,a) + \text{Extra } (h_i - h_{i-1}) \text{ columns' energy, } i=1,\dots,m$$

Step 4: Calculate the energies of the first set of regions with vertical base length v_j , ($j=1, \dots, n$) and horizontal base length h_i , ($i=1, \dots, m$) and center $(x+b, y+a)$, ($b=1, \dots, w_s$ and $a=1, \dots, h_s$) using:

$$S_{j,i}(b,a) = S_{j,i}(b-1,a) - C_{j,(hm-hi)/2+b-1}(a) + C_{j,(hm+hi)/2+b}(a)$$

- 5 The maximum modulus can be updated successively during the matching pursuit process; this can progressively confine the search space. Several bases can have the same sizes, thus one energy calculation may avoid several inner product calculations. The performance of PEA is also related with how fast a good match (not necessarily the best match) is found. Because large regions always contain more energy, bases of larger
10 dimension are tested first.

- If $\|r(k,l,p)\| > M_m$, block 86 is executed to calculate the inner product (p) between $r(k,l,p)$ and $b(k,l)$. Block 87 compares the absolute value of p with current maximum modulus M_m . If $|p| > M_m$, the new M_m is set as $|p|$ and the corresponding basis index and position
15 are recorded. Regardless, we keep returning to block 84 until all search positions have been checked. Then blocks 83 through 88 are run repeatedly until all basis candidates have been tested. Finally, an atom is produced which includes three parameters: 1. The index of basis in the dictionary that gives the best match; 2. The location of the best match in the residual image with (x, y) coordinates; and 3. The inner product (p)
20 between the basis and the residual image. Figure 12 shows an example of an atom on a residual image.

- With further reference to Figure 4, the step after finding an atom is to record the atom parameters (block 63). Note in this stage, no quantization of the atom's modulus is
25 performed. Decision block 64 will decide when to begin atom quantization. Its operation depends on the rate control goal defined by the video compression system. If the compression ratio is fixed, block 64 will check if bits are still available for more atoms. Because no actual coding has been done yet, the used bits for coding the current atoms has to be estimated. Let "Bip" represent the average bits for coding the basis
30 indices and positions, "Bm(i)" represents the actual bits for the i 'th atom's modulus without quantization. Allocating one bit for the sign of inner product (p), then the used bits for n atoms are estimated as:

$$\text{Used Bits} = n * (\text{Bip} + 1) + \sum (\text{Bm}(1) + \text{Bm}(2) + \dots \text{Bm}(n))$$

where "Bip" is initialized according to experiential data for a first residual frame, and set as real value of last frame. Bm(i) can be known exactly for each modulus. An important fact is that the modulus will be quantized later and will result in fewer bits to be used than currently estimated. Thus in this stage, there will typically be fewer atoms than what can coded. If the video system wants to achieve a certain quality, which is defined by the mean square error (MSE) of the coded residual image as compared to the actual residual image, block 64 will compare the current MSE achieved with the MSE objective. The MSE after introducing one atom is updated according to following equation:

$$\text{MSE}(n) = \text{MSE}(n-1) - p(n) * p(n)$$

where MSE(n) represents the MSE after using n atoms and p(n) represents the inner product of nth atom. Initially the MSE, or MSE(0), is set to the energy of original residual image. After quantization is performed, MSE(n) will likely increase, and therefore will no longer achieve the MSE objective. In summary, if bits are available or the quality goal has not been achieved, the residual image will be updated based on the current atom (block 65), followed by a search for another atom recommencing at block 61. Otherwise if the bit or quality objective has been achieved; block 66 is executed for the quantization design. Residual image updating, one step for the standard matching pursuit algorithm, can be described mathematically as:

$$r(k,l,p) = r(k,l,p) - p(n) * b(k,l)$$

All regions not covered by the current atom will be unchanged.

The design of the quantizer (block 66) is based on the minimum modulus (Minm) value found so far. The quantization step size (QS) is set to:

$$QS = \begin{cases} 32 & \text{if Minm} > 24; \\ 16 & \text{if } 2 < \text{Minm} \leq 24; \\ 8 & \text{if } 6 < \text{Minm} \leq 12 \\ 4 & \text{if Minm} \leq 6; \end{cases}$$

All atoms found up to this point, will be quantized using the above QS in the simple mid-read scalar quantization scheme. Next the residual image is updated again according to the now quantized list of atom moduli 67. Assume that the atom coefficient before and after quantization are $p(i)$, $q(i)$ respectively ($i=1, \dots, n$). Assume
 5 that the corresponding bases are $b(i)$, ($i=1, \dots, n$). The residual image after n unquantized atoms is:

$$E(n) = (\text{Original Residual}) - p(1)b(1) - p(2)b(2) - \dots - p(n)b(n)$$

Its energy $\|E(n)\|$ is known also. There are two ways to calculate the residual energy after quantization. The first way is to simply calculate the residual image after
 10 quantization as:

$$EQ(n) = (\text{Original Residual}) - q(1)b(1) - q(2)b(2) - \dots - q(n)b(n)$$

Another way is to update it recursively. Assume the quantization error for $p(i)$ is $\Delta p(i)$. Then the residual image with only $p(n)$ being quantized is:

$$EQ(1) = E(n) - \Delta p(n)b(n) \text{ and } \|EQ(1)\| = \|E(n)\| + \Delta p(n)^2 - 2\Delta p(n)\langle E(n), b(n) \rangle$$

15 The residual with the quantization of $p(n)$ and $p(n-1)$ becomes:

$$EQ(2) = EQ(1) - \Delta p(n-1)b(n-1)$$

This relationship is true recursively and can be written as:

$$EQ(i) = EQ(i-1) - \Delta p(n-i+1)b(n-i+1), i=1, 2, \dots, n, EQ(0) = E(n)$$

The corresponding energy is:

20 $\|EQ(i)\| = \|EQ(i-1)\| + \Delta p(n-i+1)^2 - 2\Delta p(n-i+1)\langle EQ(i-1), b(n-i+1) \rangle$

Finally, we will get $EQ(n)$ and $\|EQ(n)\|$, which is the start point for further atom finding. An important thing is that the list of atoms can be in any order for the recursive update to occur – the update does not need to occur in the order in which the atoms were found.

Because the moduli of atoms have been quantized, more atoms will now be necessary to achieve the rate control or quality objective. Therefore, block 68 is executed to find additional atoms. The process is the same as block 61 through 63. However, the atom moduli will be quantized immediately in this stage. We now need to deal with atoms
5 whose moduli is smaller than $(QS - QS/4)$, without throwing them out by setting their quantization value to zero. The scheme used is given below:

1. If the atom modulus is larger than $(QS - QS/4)$ then quantizer is using QS ;
 2. Otherwise, if the atom modulus is larger than $(QS/2 - QS/8)$ then it is quantized as
10 value $QS/2$;
 3. Otherwise, if the atom modulus is larger than $(QS/4 - QS/16)$ then it is quantized as value $QS/4$;
 4. Otherwise, if the atom modulus is larger than $(QS/8 - QS/32)$ then it is quantized as value $QS/8$.
- 15 In practice, three levels down is typically sufficient, although more levels may be used.

After block 68, a real rate control logic unit is executed (block 69). Because the atoms are quantized in-loop in this stage, the achieved quality or actual number of bits used can be estimated. When the compression goal is achieved, the system will go into the atom
20 encoder 42. Otherwise, the residual image will be updated based on the quantized atom modulus and the system will return to block 68 to find the next atom. For colour video, a residual image contains several channels, i.e. Y, U and V channels. The atom decomposer 40 will be used for each channel independently. With this scheme, each channel can have its own bit budget or desired quality goal. There are certain bit
25 allocation methods, which can be used to allocate bit budgets for the different channels.

All the atoms are passed to the atom encoder 42 for output in a compressed form. The present invention considers the atom distribution for each channel as a bi-value map, as illustrated in Figure 13. The black pixels represent atoms in their corresponding
30 position, while the white pixels represent a lack of atoms in that position. A quadtree-like technique can be used to encode the positions containing atoms, although other techniques may be used as would be readily understood. The other parameters of each atom can be encoded after the atoms position information, using variable length coding, for example, however other encoding techniques may be used as would be known to a

worker skilled in the art. The coding procedure for the atom parameter signal is illustrated in Figure 14 and described in more detail below.

The first step of atom encoding is to decompose the whole atom map, for example as illustrated in Figure 13, into $n \times n$ blocks (Block 101). The value n may either be 16 (for the Y channel) or 8 (for the U and V channels). For each $n \times n$ block, if there are no atoms in the block, a zero-bit is output; otherwise, a one-bit is output, and the block is processed further to locate the atoms to the decoder. A quadtree decomposition procedure is used for this, and is summarized in the following four steps:

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Step 1. Initialize a list of atom blocks (LAB) with one element – the $n \times n$ block itself.

Step 2. Pick one element e from LAB. If e 's size is 1×1 , output all atom parameters except for the position: namely the basis index, modulus and the sign of the inner product of e should be output, then proceed to step 4; otherwise, proceed to step

15

3.

Step 3. Output the atom pattern bits of the four sub-blocks of e : $a_1a_2a_3a_4$, where a_i ($i=1,2,3,4$) is one if there is an atom in the corresponding sub-block and zero otherwise. Put all sub-blocks i with a_i value equal to 1 into the end of the LAB and return to step 2.

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Step 4. Check if the LAB is empty. If it is not empty, return to step 2; otherwise the encoding finishes for the one $n \times n$ block.

The basis index and atom modulus can be coded using a variable length coder to conserve bits, since these signal parameters may not be uniformly distributed. The atom position information can be encoded implicitly by recording the decomposition procedure with the 0/1 bit data. A variable length coding method can be used to encode the atom pattern bits of the four sub-blocks: $a_1a_2a_3a_4$. There are 15 kinds of patterns for the atom pattern bits, $a_1a_2a_3a_4$, wherein it should be noted that 0000 is impossible. However, some patterns, such as 1000, occur with a much higher probability than other patterns. The probability of the different patterns can be estimated through experiments and used to create a variable length table design. Further, it should be noted that the probability distribution can be variable for different channels and different atom densities. Therefore multiple tables can be used, and the block's category information

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can be encoded first so the decoder knows which table should be used for decoding purposes.

Figure 15 illustrates the atom decoder 46, which performs operations that are the inverse of those performed by the atom encoder 42. First, the atom decoder 46 receives one bit representing the status for the current $n \times n$ block. If the value is one, it is processed through the symmetric quadtree decomposition procedure. Initially, the $n \times n$ block is divided into four sub-blocks. The atom pattern bits for the four sub-blocks are decoded using inverse variable length coding (VLC). Then all the sub-blocks with value 1 are put into a list of atom blocks (LAB). The LAB is updated dynamically by decomposing each element in the LAB recursively and getting its atom pattern bits. If an element from the LAB is a 1×1 block, the atom basis index and the modulus should be decoded using the inverse VLC tables; the bit representing the sign of the inner product should then be read in. The atom decoder for one $n \times n$ block is finished if the LAB becomes empty.

The decoded atom parameter signal is then passed to the residual re-constructor 48, which forms the residual image one channel by one channel using the method of classical matching pursuit. Initially all pixels on the residual image are set to zero. Then each atom is added one by one using the following procedure: Let $q(i)$ and $b(i,k,l)$ represent the i 'th atom coefficient and the corresponding 2D basis matrix respectively. If $(x(i), y(i))$ represents the location of the i 'th atom, then the matrix $q(i) \cdot b(i,k,l)$ is added to the residual image constructed so far at position $(x(i), y(i))$ to get the new current residual image. The process repeats until all atoms have been added for the channel. Once each channel has been decomposed, the process is finished and the residual image has been reconstructed.

Those familiar with the previous matching pursuit based video coding art will recognize a number of advantages associated with the techniques according to the present invention. The atom decomposition process based on an over-complete basis space has been sped up through a more accurate energy region estimation procedure and through the progressive candidate elimination algorithm. The atom modulus quantizer design is seamlessly chosen by the atom decomposition scheme, while the previous art specified the quantizer before the transformation began. Finally, the atom encoding process is

more efficient because spatial relationships between the atoms are exploited by the invented quadtree-based decomposition scheme. In particular, the prior art collects all atoms into a 1D list thereby making it harder to efficiently code them, when compared to the present invention.

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The embodiments of the invention being thus described, it will be obvious that the same may be varied in many ways. Such variations are not to be regarded as a departure from the spirit and scope of the invention, and all such modifications as would be obvious to one skilled in the art are intended to be included within the scope of the following

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claims.